

15	3053	80.3	737	2	Q6NU15_XENLA	Q6nu15 xenopus lae
16	3053	80.3	769	2	Q7ZWS3_XENLA	Q7zws3 xenopus lae
17	2541.5	66.8	729	2	Q9PVF7_BRARE	Q9pvf7 brachydanio
18	2487	65.4	781	2	Q63ZT4_XENLA	Q63zt4 xenopus lae
19	2485	65.3	781	1	CTNB1_HUMAN	P35222 homo sapien
20	2485	65.3	781	2	Q8WNW4_PIG	Q8wnw4 sus scrofa
21	2485	65.3	781	2	Q5R5L8_PONPY	Q5r5l8 pongo pygma
22	2485	65.3	781	2	Q28GC2_XENTR	Q28gc2 xenopus tro
23	2484	65.3	774	2	Q4R3D3_MACFA	Q4r3d3 macaca fasc
24	2484	65.3	781	2	Q5R2I4_TRISI	Q5r2i4 trionyx sin
25	2483	65.3	781	2	Q7ZX35_XENLA	Q7zx35 xenopus lae
26	2482	65.2	781	1	CTNB1_RAT	Q9wu82 rattus norv
27	2482	65.2	781	2	Q76LW0_MERUN	Q76lw0 meriones un
28	2481	65.2	781	1	CTNB1_MOUSE	Q02248 mus musculu
29	2481	65.2	781	1	CTNB_XENLA	P26233 xenopus lae
30	2479	65.2	781	2	Q3UZT7_MOUSE	Q3uzt7 mus musculu
31	2474	65.0	781	2	O42486_CHICK	O42486 gallus gall
32	2465	64.8	778	2	Q8JID2_BRARE	Q8jid2 brachydanio
33	2452.5	64.5	780	2	Q7ZU14_BRARE	Q7zul4 brachydanio
34	2452.5	64.5	780	2	Q7T192_CARAU	Q7t192 carassius a
35	2450.5	64.4	780	2	Q90424_BRARE	Q90424 brachydanio
36	2442.5	64.2	753	2	Q4T227_TETNG	Q4t227 tetraodon n
37	2436.5	64.1	801	2	Q4RFE6_TETNG	Q4rfe6 tetraodon n
38	2376.5	62.5	793	2	Q4SUZ0_TETNG	Q4suz0 tetraodon n
39	2376	62.5	701	2	Q5ISL3_MACFA	Q5isl3 macaca fasc
40	2349	61.8	816	2	Q8WRT5_CHAVR	Q8wrt5 chaetopteru
41	2315.5	60.9	860	2	Q4U478_BRAFL	Q4u478 branchiosto
42	2312.5	60.8	860	2	Q75WV7_BRABE	Q75wv7 branchiosto
43	2259.5	59.4	821	2	Q75WU5_ACHTE	Q75wu5 achaearanae
44	2217.5	58.3	769	2	Q4H3U7_CIOIN	Q4h3u7 ciona intes
45	2214.5	58.2	769	2	Q9NL44_CIOIN	Q9nl44 ciona intes

## ALIGNMENTS

## RESULT 1

## Q15151\_HUMAN

ID Q15151\_HUMAN PRELIMINARY; PRT; 745 AA.  
AC Q15151; Q15093;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 25-JUL-2006, entry version 36.  
DE Plakoglobin.  
GN Name=JUP;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
OC Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=89264555; PubMed=2726765;  
RA Franke W.W., Goldschmidt M.D., Zimbelmann R., Mueller H.M.,  
RA Schiller D.L., Cowin P.;  
RT "Molecular cloning and amino acid sequence of human plakoglobin, the  
RT common junctional plaque protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:4027-4031(1989).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Zimbelmann R.;  
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20469067; PubMed=11016852;  
RX DOI=10.1034/j.1600-0625.2000.009005323.x;  
RA Whittock N.V., Eady R.A.J., McGrath J.A.;  
RT "Genomic Organization and amplification of the human plakoglobin  
RT gene.";  
RL Exp. Dermatol. 9:323-326(2000).  
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CC -----  
DR EMBL; Z68228; CAA92522.1; -; mRNA.  
DR EMBL; AF306723; AAG16727.1; -; Genomic\_DNA.

DR EMBL; AF233882; AAG16727.1; JOINED; Genomic\_DNA.  
 DR UniGene; Hs.514174; -.  
 DR HSSP; Q02248; 2BCT.  
 DR SMR; Q15151; 142-653.  
 DR Ensembl; ENSG00000173801; Homo sapiens.  
 DR RZPD-ProtExp; A0385; -.  
 DR RZPD-ProtExp; IOH29325; -.  
 DR GO; GO:0005488; F:binding; IEA.  
 DR InterPro; IPR011989; ARM-like.  
 DR InterPro; IPR000225; Armadillo.  
 DR InterPro; IPR013284; Beta-catenin.  
 DR InterPro; IPR000357; HEAT.  
 DR Pfam; PF00514; Arm; 6.  
 DR Pfam; PF02985; HEAT; 1.  
 DR PRINTS; PR01869; BCATNINFAMILY.  
 DR SMART; SM00185; ARM; 7.  
 DR PROSITE; PS50176; ARM\_REPEAT; 7.  
 KW Cell adhesion; Repeat; Structural protein.  
 SQ SEQUENCE 745 AA; 81745 MW; 3519A0973748BCF4 CRC64;

Query Match 100.0%; Score 3804; DB 2; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-219;  
 Matches 745; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEVMNLMEQPIKVTWQQTYTYDSGIHSGANTCVPSVSSKGIMEEDEACGRQYTLKKT	60
Db	1	MEVMNLMEQPIKVTWQQTYTYDSGIHSGANTCVPSVSSKGIMEEDEACGRQYTLKKT	60
Qy	61	YTQGVPPSQGDLEYQMSTTARAKRVREAMCPGVSGEDSSLLLATQVEGQATNLQRLAEP	120
Db	61	YTQGVPPSQGDLEYQMSTTARAKRVREAMCPGVSGEDSSLLLATQVEGQATNLQRLAEP	120
Qy	121	QLLKSAIVHLINQDDAELATRALPELTCLLNDEDPVVVTKAAMIVNQLSKKEASRRALM	180
Db	121	QLLKSAIVHLINQDDAELATRALPELTCLLNDEDPVVVTKAAMIVNQLSKKEASRRALM	180
Qy	181	GSPQLVAAVVRTMQNTSDLDTARCTTSILHNLSSHREGLLAIFKSGGIPALVRMLSSPVE	240
Db	181	GSPQLVAAVVRTMQNTSDLDTARCTTSILHNLSSHREGLLAIFKSGGIPALVRMLSSPVE	240
Qy	241	SVLFYAITTLHNLLLYQEGAKMAVRLADGLQKMVPLLNKNNPKFLAITTDCLQLLAYGNQ	300
Db	241	SVLFYAITTLHNLLLYQEGAKMAVRLADGLQKMVPLLNKNNPKFLAITTDCLQLLAYGNQ	300
Qy	301	ESKLIILANGGPQALVQIMRNYSYEKLLWTTSRVLKVLVSVCPNPKPAIVEAGGMQALGKH	360
Db	301	ESKLIILANGGPQALVQIMRNYSYEKLLWTTSRVLKVLVSVCPNPKPAIVEAGGMQALGKH	360
Qy	361	LTSNSPRLVQNCWLRLNLSVATKQEGLESVLKILVNQLSVDDVNVLTGATGTLNLT	420
Db	361	LTSNSPRLVQNCWLRLNLSVATKQEGLESVLKILVNQLSVDDVNVLTGATGTLNLT	420
Qy	421	NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLSRHPAEMAQNSVRLNY	480
Db	421	NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLSRHPAEMAQNSVRLNY	480
Qy	481	GIPAIVKLLNQPNQWPLVKATIGLIRNLALCPANHAPLQEA AVIPRLVQLLVKAHQDAQ	540
Db	481	GIPAIVKLLNQPNQWPLVKATIGLIRNLALCPANHAPLQEA AVIPRLVQLLVKAHQDAQ	540
Qy	541	HVAAGTQQPYTDGVRMEEIVEGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSVENI	600
Db	541	HVAAGTQQPYTDGVRMEEIVEGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSVENI	600
Qy	601	QRVAAGVLCELAQDKEADAIDAEGASAPLMELLHSRNEGATATYAAAVLFRISEDKNPDY	660
Db	601	QRVAAGVLCELAQDKEADAIDAEGASAPLMELLHSRNEGATATYAAAVLFRISEDKNPDY	660
Qy	661	RRKRVSVELTNSLFKHDPAAWAAQSMIPINEPYGDDMDATYRPMYSSDVPLDPLEMHMDM	720
Db	661	RRKRVSVELTNSLFKHDPAAWAAQSMIPINEPYGDDMDATYRPMYSSDVPLDPLEMHMDM	720
Qy	721	DGDYPIDTYS DGLRPPYPTADHMLA	745
Db	721	DGDYPIDTYS DGLRPPYPTADHMLA	745